SEQUENCE LISTING

<110> Zeneca Limited

<120> Insecticidal Proteins from Paecilomyces and Synergistic Combinations Thereof

<130> SYN-128

<140> PCT/GB00/02457
<141> 2000-06-23

<150> GB 9915215.9
<151> 1999-06-29

<150> GB 9930536.9
<151> 1999-12-23

<160> 65

<170> FastSEQ for Windows Version 4.0

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<212> PRT
<213> Paecilomyces sp.

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<222> 1, 2
<223> Xaa = Any Amino Acid

<221> VARIANT
<222> 1, 2
<223> Xaa = Any Amino Acid

<400> 1
Xaa Xaa Ile Cys Thr Pro Ala Gly Val Lys Cys Pro Ala Ala Leu Pro
 1   5   10   15
Cys Cys Pro Gly Leu Arg Cys Ile Gly Gly Val Asn Asn Lys Val Cys
            20   25   30
Arg

<210> 2
<211> 33
<212> PRT
<213> Paecilomyces sp.

<400> 2
Gly Lys Ile Cys Thr Pro Ala Gly Val Lys Cys Pro Ala Ala Leu Pro
 1   5   10   15
Cys Cys Pro Gly Leu Arg Cys Ile Gly Gly Val Asn Asn Lys Val Cys
            20   25   30
Arg

<210> 3
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<213> Paecilomyces sp.

<220>
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<221> VARIANT
<222> 1, 2
<223> Xaa = Any Amino Acid

<400> 3
Xaa Xaa Gly Lys Ile Cys Thr Pro Ala Gly Val Lys Cys Pro Ala Ala
 1   5   10   15
Leu Pro Cys Cys Pro Gly Leu Arg Cys Ile Gly Gly Val Asn Asn Lys
            20   25   30
Val Cys Arg
        35

<210> 4
<211> 332
<212> DNA
<213> Paecilomyces sp.

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tctaacatga agcaactttc tcttctctct agaaatgtcc cgcggctctt ccttgctgcc 120
ccggacttcg ctgcatcggc ggcgtcaacg taagtcacca tggatctggc aagcgagacc 180
ataacatgac gcagtatact aaccctggcc gttatagaac aaggttgtga gtcgacatgt 240
tktacaacct ctacaaacgc gcgcactaat gacaacggta gtgccggtaa ttctagtgtc 300
gcaacttttg agcgtgggat aagtatgctt cg   332

<210> 5
<211> 320
<212> DNA
<213> Paecilomyces sp.

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gggaaaattt gtacgccggc gggggttgta cgtattctca tccatttcct ccaccactcc 60
tctaacatga agcaactctc tcttctctct agaaatgtcc cgcggctctt ccttgctgcc 120
ccggacttcg ctgcatcggc ggcgtcaacg taagtcacca tcctgacacg acgtgaaggc 180
aatgtactga ccctggccgt tatagaacaa ggttgtgagt cgacatgttt tacaacctct 240
acaaacgcgc gcactaatga caacggtagt gccggtaatt ctagtgtcgc aacttttgag 300
cgtgggataa gtatgcttcg   320

<210> 6
<211> 320
<212> DNA
<213> Paecilomyces sp.

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gggaaaatct gtacgccggc gggggttgta cgtattttca tccatttcct ccaccactcc 60

tctaacatga agcaactctc tcttctctct araaatgtcc cgcggctctt ccttgctgcc 120
ccggacttcg ctgcatcggc ggcgtcaacg taagtcacca tcctgacacg acgtgaaggc 180
aatgtactga ccctggccgt tatagaacaa ggttgtgagt cgacatgttt tacaacctct 240
acaaacgcgc gcactaatga caacggtagt gccggtaatt ctagtgtcgc aacttttgag 300
cgtgggataa gtatgcttcg 320

<210> 7
<211> 174
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide codon optimised

<400> 7
atgggtggca gcggcagggc tgctctgctg ctggccctgg tggccgtgag cctggccgtg 60
gagatccagg ccggcaagat ctgcaccccg gccggcgtga agtgcccggc cgccctcccg 120
tgctgcccgg gcctccgctg catcggcggc gtgaacaaca aggtgtgccg ctga 174

<210> 8
<211> 174
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide codon optimised

<400> 8
atgggtggca gcggcagggc tgctctgctg ctggccctgg tggccgtgag cctggccgtg 60
gagatccagg ccggtaaaat ttgtaccccg gccggcgtga agtgcccggc cgccctcccg 120
tgttgtccgg gcctcaggtg tattggtggt gtgaataata aagtgtgtcg ctga 174

<210> 9
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence containing intron sequence

<400> 9
atgggtggca gcggcagggc tgctctgctg ctggccctgg tggccgtgag cctggccgtg 60
gagatccagg ccggcaagat ctgcactcct gctggagttg tttgtttctg cttctacctt 120
tgatatatat ataataatta tcattaatta gtagtaatat aatatttcaa atatttttttt 180
caaaataaaa gaatgtagta tatagcaatt gcttttctgt agtttataag tgtgtatatt 240
ttaatttata acttttctaa tatatgacca aaacatggtg atgtttagaa atgtcccgcg 300
gctcttcctt gctgccccgg acttcgctgc atcggcggcg tcaacaacaa ggtttgccgg 360
taa 363

<210> 10
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence

<400> 10
atgggtggca gcggcagggc tgctctgctg ctggccctgg tggccgtgag cctggccgtg 60
gagatccagg cctcctacgg caagatctgc actcctgctg gagttgtttg tttctgcttc 120
tacctttgat atatatataa taattatcat taattagtag taatataata tttcaaatat 180
ttttttcaaa ataaaagaat gtagtatata gcaattgctt ttctgtagtt tataagtgtg 240
tatattttaa tttataactt ttctaatata tgaccaaaac atggtgatgt ttagaaatgt 300
cccgcggctc ttccttgctg ccccggactt cgctgcatcg gcggcgtcaa caacaaggtt 360
tgccggtaa 369

<210> 11
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence

<400> 11
atgggtggca gcggcagggc tgctctgctg ctggccctgg tggccgtgag cctggccgtg 60
gagatccagg cctcctacat ctgcactcct gctggagttg tttgtttctg cttctacctt 120
tgatatatat ataataatta tcattaatta gtagtaatat aatatttcaa atatttttt 180
caaaataaaa gaatgtagta tatagcaatt gcttttctgt agtttataag tgtgtatatt 240
ttaatttata acttttctaa tatatgacca aaacatggtg atgtttagaa atgtcccgcg 300
gctcttcctt gctgccccgg acttcgctgc atcggcggcg tcaacaacaa ggtttgccgg 360
taa 363

<210> 12
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence containing intron and codon
optimised

<400> 12
atgggtggca gcggcagggc tgctctgctg ctggccctgg tggccgtgag cctggccgtg 60
gagatccagg ccggcaagat ctgcaccccg gccggcgtgg tttgtttctg cttctacctt 120
tgatatatat ataatattta tcattaatta gtagtaatat aatatttcaa atatttttt 180
caaaataaaa gaatgtagta tatagcaatt gcttttctgt agtttataag tgtgtatatt 240
ttaatttata acttttctaa tatatgacca aaacatggtg atgtttagaa gtgcccggcc 300
gccctcccgt gctgcccggg cctccgctgc atcggcggcg tgaacaacaa ggtgtgccgc 360
tga 363

<210> 13
<211> 439
<212> DNA
<213> Paecilomyces sp.

<400> 13
tctacttctt catctcacgc catatatcct cccaaaatca cacctcttcc ttcaccatgc 60
aaatctccgc cgtcattgtc gcactcttcg ccagcgccgc catggccggc aagatctgca 120
ctcctgctgg agttgtacgt attttcatcc atttcctyca ccactcctct aacatgaagc 180
aactttctct tctctctaga aatgtcccgc ggctcttcct tgctgccccg gacttcgctg 240
catcggcggc gtcaacgtaa gtcaccatgg atctggcaag cgagaccata acatgacgca 300
gtatactaac cctggccgtt atagaacaag gttgtgagtc gacatgttkt acaacctcta 360
caaacgcgcg cactaatgac aacggtagtg ccggtaattc tagtgtcgca acttttgagc 420

gtgggataag tatgcttcg 439

<210> 14
<211> 102
<212> DNA
<213> Paecilomyces sp.

<400> 14
ggcaagatct gcactcctgc tggagttaaa tgtcccgcgg ctcttccttg ctgccccgga 60
cttcgctgca tcggcggcgt caacaacaag gtttgccggt aa 102

<210> 15
<211> 84
<212> DNA
<213> Dahlia sp.

<400> 15
atggttaata gatctgttgc tttttctgct tttgttctta ttctttttgt tttggctatt 60
tcagatattg cttctgtttc agga 84

<210> 16
<211> 87
<212> DNA
<213> Artificial Sequence

<220>
<223> Radish signal sequence

<400> 16
atggctaagt ttgcttctat tattgctctt ttgtttgctg cacttgtttt gtttgctgca 60
tttgaagctc caactatggt tgaagct 87

<210> 17
<211> 72
<212> DNA
<213> Zea mays

<400> 17
atgggtggca gcggcagggc tgctctgctg ctggccctgg tggccgtgag cctggccgtg 60
gagatccagg cc 72

<210> 18
<211> 90
<212> DNA
<213> Nicotiana sp.

<400> 18
atgggatttg ttctcttttc acaattgcct tcatttcttc ttgtctctac acttctctta 60
ttcctagtaa tatcccactc ttgccgtgcc 90

<210> 19
<211> 51
<212> DNA
<213> Paecilomyces sp.

<400> 19
atgcaaatct ccgccgtcat tgtcgcactc ttcgccagcg ccgccatggc c 51

<210> 20
<211> 28
<212> PRT
<213> Dahlia sp.

<400> 20
Met Val Asn Arg Ser Val Ala Phe Ser Ala Phe Val Leu Ile Leu Phe
 1   5   10   15
Val Leu Ala Ile Ser Asp Ile Ala Ser Val Ser Gly
            20   25

<210> 21
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
<223> Radish protein target sequence

<400> 21
Met Ala Lys Phe Ala Ser Ile Ile Ala Leu Leu Phe Ala Ala Leu Val
 1   5   10   15
Leu Phe Ala Ala Phe Glu Ala Pro Thr Met Val Glu Ala
            20   25

<210> 22
<211> 24
<212> PRT
<213> Zea Mays

<400> 22
Met Gly Gly Ser Gly Arg Ala Ala Leu Leu Leu Ala Leu Val Ala Val
 1   5   10   15
Ser Leu Ala Val Glu Ile Gln Ala
            20

<210> 23
<211> 30
<212> PRT
<213> Nicotiana sp.

<400> 23
Met Gly Phe Val Leu Phe Ser Gln Leu Pro Ser Phe Leu Leu Val Ser
 1   5   10   15
Thr Leu Leu Leu Phe Leu Val Ile Ser His Ser Cys Arg Ala
            20   25   30

<210> 24
<211> 17
<212> PRT
<213> Paecilomyces sp.

<400> 24

Met Gln Ile Ser Ala Val Ile Val Ala Leu Phe Ala Ser Ala Ala Met
1 5 10 15
Ala

<210> 25
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Primers

<400> 25
tcgggctcgc atgaattcgc ggccgcattt ttttttttt tttt 44

<210> 26
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Primers

<400> 26
tcgggctcgc atgaattcg 19

<210> 27
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Primers

<400> 27
atgaattcgc ggccgcat 18

<210> 28
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primers

<400> 28
tcgggctcgc atgaattcgc g 21

<210> 29
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
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<400> 29
ctcgcatgaa ttcgcggccg c 21

<210> 30
<211> 17
<212> RNA
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<220>
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<221> misc_feature
<222> 9, 12, 15
<223> n = A,T,C or G

<221> misc_feature
<222> 9, 12, 15
<223> n = A,T,C or G

<400> 30
athtgyacnc cngcngg 17

<210> 31
<211> 20
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<221> misc_feature
<222> 9, 12, 15, 18
<223> n = A,T,C or G

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<222> 9, 12, 15, 18
<223> n = A,T,C or G

<400> 31
athtgyacnc cngcnggngt 20

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<221> misc_feature
<222> 3, 6, 9, 12, 15
<223> n = A,T,C or G

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<400> 32
acnccngcng gngtnaa 17

<210> 33
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<221> misc_feature
<222> 3, 12, 15
<223> n = A,T,C or G

<221> misc_feature
<222> 3, 12, 15
<223> n = A,T,C or G

<400> 33
ccntgytgyc cnggnyt 17

<210> 34
<211> 16
<212> RNA
<213> Artificial Sequence

<220>
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<221> misc_feature
<222> 2, 14
<223> n = A,T,C or G

<221> misc_feature
<222> 2, 14
<223> n = A,T,C or G

<400> 34
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<210> 35
<211> 20
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<221> misc_feature
<222> 3, 6, 18
<223> n = A,T,C or G

<221> misc_feature
<222> 3, 6, 18
<223> n = A,T,C or G

<400> 35
ggngtnaaya ayaargtntg 20

<210> 36
<211> 26
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<213> Artificial Sequence

<220>
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<221> misc_feature
<222> 12, 15, 18, 21, 24
<223> n = inosine

<400> 36
aarathtgya cnccngcngg ngtnaa 26

<210> 37
<211> 26
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<220>
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<221> misc_feature
<222> 3, 6, 9, 12, 21, 24
<223> n = inosine

<400> 37
ccngcnggng tnaartgycc ngcngc 26

<210> 38
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
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<221> misc_feature
<222> 6, 9, 12, 15, 18
<223> n = inosine

<400> 38
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<210> 39
<211> 26
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<220>
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<221> misc_feature

<222> 9, 12, 15
<223> n = inosine

<400> 39
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<210> 40
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<400> 40
taaatgtccc gcggctcttc c 21

<210> 41
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<220>
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<400> 41
cggctcttcc ttgctgcccc g 21

<210> 42
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
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<400> 42
tgctgccccg gacttcgctg c 21

<210> 43
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<221> misc_feature
<222> 23, 24, 25, 26, 27
<223> n = A,T,C or G

<221> misc_feature
<222> 23, 24, 25, 26, 27
<223> n = A,T,C or G

<400> 43
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<210> 44
<211> 22
<212> DNA
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<220>
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<400> 44
ctcaaacttg ggtaattaaa cc 22

<210> 45
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
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<400> 45
ggtttaatta cccaagtt 18

<210> 46
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
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<400> 46
taattaccca agtttgag 18

<210> 47
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
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<400> 47
ggtttaatta cccaagtttg ag 22

<210> 48
<211> 23
<212> DNA
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<221> misc_feature
<222> 3, 15, 18, 21
<223> n = inosine

<400> 48

canacyttrt trttnacncc ncc 23

<210> 49
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<220>
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<400> 49
atgcagcgaa gtccggggca g 21

<210> 50
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<400> 50
ggggcagcaa ggaagagccg c 21

<210> 51
<211> 21
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<213> Artificial Sequence

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<400> 51
aagagccgcg ggacatttaa c 21

<210> 52
<211> 49
<212> DNA
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<220>
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<400> 52
agttaaatgt cccgcggctc ttccttgctg ccccggactt cgctgcatc 49

<210> 53
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Primers

<400> 53
gatgcagcga agtccggg 18

<210> 54
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<212> PRT
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<220>
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<222> 602
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<221> VARIANT
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<400> 54

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Met Lys Leu Lys Asn Gln Asp Lys His Gln Ser Phe Ser Ser Asn Ala
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Lys Val Asp Lys Ile Ser Thr Asp Ser Leu Lys Asn Glu Thr Asp Ile
            20                  25                  30
Glu Leu Gln Asn Ile Asn His Glu Asp Cys Leu Lys Met Ser Glu Tyr
        35                  40                  45
Glu Asn Val Glu Pro Phe Val Ser Ala Ser Thr Ile Gln Thr Gly Ile
    50                  55                  60
Gly Ile Ala Gly Lys Ile Leu Gly Thr Leu Gly Val Pro Phe Ala Gly
65                  70                  75                  80
Gln Val Ala Ser Leu Tyr Ser Phe Ile Leu Gly Glu Leu Trp Pro Lys
                85                  90                  95
Gly Lys Asn Gln Trp Glu Ile Phe Met Glu His Val Glu Glu Ile Ile
            100                 105                 110
Asn Gln Lys Ile Ser Thr Tyr Ala Arg Asn Lys Ala Leu Thr Asp Leu
        115                 120                 125
Lys Gly Leu Gly Asp Ala Leu Ala Val Tyr His Asp Ser Leu Glu Ser
    130                 135                 140
Trp Val Gly Asn Arg Asn Asn Thr Arg Ala Arg Ser Val Val Lys Ser
145                 150                 155                 160
Gln Tyr Ile Ala Leu Glu Leu Met Phe Val Gln Lys Leu Pro Ser Phe
                165                 170                 175
Ala Val Ser Gly Glu Glu Val Pro Leu Leu Pro Ile Tyr Ala Gln Ala
            180                 185                 190
Ala Asn Leu His Leu Leu Leu Leu Arg Asp Ala Ser Ile Phe Gly Lys
        195                 200                 205
Glu Trp Gly Leu Ser Ser Ser Glu Ile Ser Thr Phe Tyr Asn Arg Gln
    210                 215                 220
Val Glu Arg Ala Gly Asp Tyr Ser Tyr His Cys Val Lys Trp Tyr Ser
225                 230                 235                 240
Thr Gly Leu Asn Asn Leu Arg Gly Thr Asn Ala Glu Ser Trp Val Arg
                245                 250                 255
Tyr Asn Gln Phe Arg Arg Asp Met Thr Leu Met Val Leu Asp Leu Val
            260                 265                 270
Ala Leu Phe Pro Ser Tyr Asp Thr Gln Met Tyr Pro Ile Lys Thr Thr
        275                 280                 285
Ala Gln Leu Thr Arg Glu Val Tyr Thr Asp Ala Ile Gly Thr Val His
    290                 295                 300
Pro His Pro Ser Phe Thr Ser Thr Thr Trp Tyr Asn Asn Asn Ala Pro
305                 310                 315                 320
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Ser Phe Ser Ala Ile Glu Ala Ala Val Val Arg Asn Pro His Leu Leu
                325                 330                 335
Asp Phe Leu Glu Gln Val Thr Ile Tyr Ser Leu Leu Ser Arg Trp Ser
            340                 345                 350
Asn Thr Gln Tyr Met Asn Met Trp Gly Gly His Lys Leu Glu Phe Arg
        355                 360                 365
Thr Ile Gly Gly Thr Leu Asn Ile Ser Thr Gln Gly Ser Thr Asn Thr
    370                 375                 380
Ser Ile Asn Pro Val Thr Leu Pro Phe Thr Ser Arg Asp Val Tyr Arg
385                 390                 395                 400
Thr Glu Ser Leu Ala Gly Leu Asn Leu Phe Leu Thr Gln Pro Val Asn
                405                 410                 415
Val Pro Arg Val Asp Phe His Trp Lys Phe Val Thr His Pro Ile Ala
            420                 425                 430
Ser Asp Asn Phe Tyr Tyr Pro Gly Tyr Ala Gly Ile Gly Thr Gln Leu
        435                 440                 445
Gln Asp Ser Glu Asn Glu Leu Pro Pro Glu Ala Thr Gly Gln Pro Asn
    450                 455                 460
Tyr Glu Ser Tyr Ser His Arg Leu Ser His Ile Gly Leu Ile Ser Ala
465                 470                 475                 480
Ser His Val Lys Ala Leu Val Tyr Ser Trp Thr His Arg Ser Ala Asp
                485                 490                 495
Arg Thr Asn Thr Ile Glu Pro Asn Ser Ile Thr Gln Ile Pro Leu Val
            500                 505                 510
Lys Ala Phe Asn Leu Ser Ser Gly Ala Ala Val Val Arg Gly Pro Gly
        515                 520                 525
Phe Thr Gly Gly Asp Ile Leu Arg Arg Thr Asn Thr Gly Thr Phe Gly
    530                 535                 540
Asp Ile Arg Val Asn Ile Asn Pro Pro Phe Ala Gln Arg Tyr Arg Val
545                 550                 555                 560
Arg Ile Arg Tyr Ala Ser Thr Thr Asp Leu Gln Phe His Thr Ser Ile
                565                 570                 575
Asn Gly Lys Ala Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Asn Arg
            580                 585                 590
Gly Glu Asp Leu Asp Tyr Lys Thr Phe Xaa Thr Val Gly Phe Thr Thr
        595                 600                 605
Pro Phe Ser Leu Leu Asp Val Gln Ser Thr Phe Thr Ile Gly Ala Trp
    610                 615                 620
Asn Phe Ser Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe Val
625                 630                 635                 640
Pro Val Glu Val Thr Tyr Glu Ala Glu Tyr Asp Phe Glu Lys Ala Gln
                645                 650                 655
Glu Lys Val Thr Ala Leu Phe Thr Ser Thr Asn Pro Arg Gly Leu Lys
            660                 665                 670
Thr Asp Val Lys Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val Glu
        675                 680                 685
Ser Leu Ser Asp Glu Phe Tyr Leu Asp Glu Lys Arg Glu Leu Phe Glu
    690                 695                 700
Ile Val Lys Tyr Ala Lys Gln Leu His Ile Glu Arg Asn Met
705                 710                 715
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<210> 55
<211> 719
<212> PRT
<213> Artificial Sequence

<220>
<223> PROTEIN cry1Ia2 Embl. Accession No. M98544

<400> 55

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Met Lys Leu Lys Asn Gln Asp Lys His Gln Ser Phe Ser Ser Asn Ala
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Lys Val Asp Lys Ile Ser Thr Asp Ser Leu Lys Asn Glu Thr Asp Ile
            20                  25                  30
Glu Leu Gln Asn Ile Asn His Glu Asp Cys Leu Lys Met Ser Glu Tyr
        35                  40                  45
Glu Asn Val Glu Pro Phe Val Ser Ala Ser Thr Ile Gln Thr Gly Ile
    50                  55                  60
Gly Ile Ala Gly Lys Ile Leu Gly Thr Leu Gly Val Pro Phe Ala Gly
65                  70                  75                  80
Gln Val Ala Ser Leu Tyr Ser Phe Ile Leu Gly Glu Leu Trp Pro Lys
                85                  90                  95
Gly Lys Asn Gln Trp Glu Ile Phe Met Glu His Val Glu Glu Ile Ile
            100                 105                 110
Asn Gln Lys Ile Ser Thr Tyr Ala Arg Asn Lys Ala Leu Thr Asp Leu
        115                 120                 125
Lys Gly Leu Gly Asp Ala Leu Ala Val Tyr His Asp Ser Leu Glu Ser
    130                 135                 140
Trp Val Gly Asn Arg Asn Asn Thr Arg Ala Arg Ser Val Val Lys Ser
145                 150                 155                 160
Gln Tyr Ile Ala Leu Glu Leu Met Phe Val Gln Lys Leu Pro Ser Phe
                165                 170                 175
Ala Val Ser Gly Glu Glu Val Pro Leu Leu Pro Ile Tyr Ala Gln Ala
            180                 185                 190
Ala Asn Leu His Leu Leu Leu Leu Arg Asp Ala Ser Ile Phe Gly Lys
        195                 200                 205
Glu Trp Gly Leu Ser Ser Ser Glu Ile Ser Thr Phe Tyr Asn Arg Gln
    210                 215                 220
Val Glu Arg Ala Gly Asp Tyr Ser Asp His Cys Val Lys Trp Tyr Ser
225                 230                 235                 240
Thr Gly Leu Asn Asn Leu Arg Gly Thr Asn Ala Glu Ser Trp Val Arg
                245                 250                 255
Tyr Asn Gln Phe Arg Arg Asp Met Thr Leu Met Val Leu Asp Leu Val
            260                 265                 270
Ala Leu Phe Pro Ser Tyr Asp Thr Gln Met Tyr Pro Ile Lys Thr Thr
        275                 280                 285
Ala Gln Leu Thr Arg Glu Val Tyr Thr Asp Ala Ile Gly Thr Val His
    290                 295                 300
Pro His Pro Ser Phe Thr Ser Thr Thr Trp Tyr Asn Asn Asn Ala Pro
305                 310                 315                 320
Ser Phe Ser Ala Ile Glu Ala Ala Val Val Arg Asn Pro His Leu Leu
                325                 330                 335
Asp Phe Leu Glu Gln Val Thr Ile Tyr Ser Leu Leu Ser Arg Trp Ser
            340                 345                 350
Asn Thr Gln Tyr Met Asn Met Trp Gly Gly His Lys Leu Glu Phe Arg
        355                 360                 365
Thr Ile Gly Gly Thr Leu Asn Ile Ser Thr Gln Gly Ser Thr Asn Thr
    370                 375                 380
Ser Ile Asn Pro Val Thr Leu Pro Phe Thr Ser Arg Asp Val Tyr Arg
385                 390                 395                 400
Thr Glu Ser Leu Ala Gly Leu Asn Leu Phe Leu Thr Gln Pro Val Asn
                405                 410                 415
Gly Val Pro Arg Val Asp Phe His Trp Lys Phe Val Thr His Pro Ile
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                420                 425                 430
Ala Ser Asp Asn Phe Tyr Tyr Pro Gly Tyr Ala Gly Ile Gly Thr Gln
        435                 440                 445
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